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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/841,720A

DATE: 12/05/2001
TIME: 15:07:25

Input Set : N:\Crf3\RULE60\09841720A.RAW
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SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: Yu, Lei
     7
            (ii) TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSOTIONS AND
                                     METHODS
      8
           (iii) NUMBER OF SEQUENCES: 9
     10
            (iv) CORRESPONDENCE ADDRESS:
     12
                  (A) ADDRESSEE: Arnold, White & Durkee
     13
                  (B) STREET: P.O. Box 4433
     14
                                                         ENTERED
     15
                  (C) CITY: Houston
                  (D) STATE: Texas
     16
     17
                  (E) COUNTRY: USA
     18
                  (F) ZIP: 77210
             (v) COMPUTER READABLE FORM:
     20
     21
                  (A) MEDIUM TYPE: Floppy disk
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                  (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     23
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     24
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/841,720A
C--> 27
                  (B) FILING DATE: 24-Apr-2001
C--> 28
     29
                  (C) CLASSIFICATION: 435
     31
           (vii) PRIOR APPLICATION DATA:
                  (A) APPLICATION NUMBER: 08/120,601
     32
     33
                  (B) FILING DATE: 1993-09-13
          (viii) ATTORNEY/AGENT INFORMATION:
     36
                  (A) NAME: Wilson, Mark B.
     37
                  (B) REGISTRATION NUMBER: 37,259
                  (C) REFERENCE/DOCKET NUMBER: INDA:002
     38
     40
            (ix) TELECOMMUNICATION INFORMATION:
     41
                  (A) TELEPHONE: 512/418-3000
                  (B) TELEFAX: 512/474-7577
     42
     45 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
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                  (A) LENGTH: 1618 base pairs
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     49 .
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: single
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                  (D) TOPOLOGY: linear
            (ix) FEATURE:
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                  (A) NAME/KEY: CDS
                  (B) LOCATION: 214..1407
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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84 Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile 85 60 65 70	
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133 250 255 260	

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	Thr	Phe	Gln		Val	Ser	Trp	His		Cys	Ile	Ala	Leu		тyr	Thr	
149				315					320				a	325		mma	1040
												CTG					1242
	Asn	Ser	_	Leu	Asn	Pro	val		туг	Ala	Pne	Leu		Glu	ASN	Pne	
153		993	330	mma		63.6	mma	335	3.00	003	* ~ ~	maa	340	3.00	3.00	CAA	1200
												TCG					1290
	гаг	-	Cys	Pne	Arg	GIU		Cys	TIE	PIO	THI	Ser	ser	TIII	116	GIU	
157	CAC	345	330	mcc	A CITI	CCA	350	CCT	CAC	220	A CITI	355 AGG	CNN	C N ITT	CCC	TICC.	1338
												Arg					1330
	360	GIII	ASII	ser	TilT	365	Val	AIG	GIII	ASII	370	AIG	GIU	птъ	PIO	375	
		сст	ייי א א	$\lambda \subset \lambda$	CTC		CGA	አ ርጥ	אאר	CAC		CTA	CAA	ል ል ጥ	СТС		1386
												Leu					1300
165	1111	пта	ASII	1111	380	АЗР	nr 9	T 111	No!!	385	GIII	шси	Olu	non	390	Olu	
	GCA	GAA	АСТ	GCT		ጥጥር	CCC	ТΑΑС	TTGGG		CAC	ACCAT	rc cz	AGAC		÷	1437
	Ala							11111	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		. 01101						
							Pro										
			1		FIO	цец	Pro										
169				395				rgga <i>i</i>	A TC	AGGT	GCT	GTC	AGGG!	rgt (GTGG	SAGGCT	1497
169 171	CTA	AGCT	rag 1	395 AGGC(CGCCI	AT CI	racgi									SAGGCT ACTTCA	1497 1557
169 171 173	CTA!	AGCT!	TAG A	395 AGGC(GAGA <i>l</i>	CGCCI	AT CI	racgi rgato	CCTG	AT:	rcaa <i>i</i>	AGTC	ATTO	CCTC	rct (GCT		
169 171 173	CTAA CTGC	AGCT!	TAG A	395 AGGC(GAGA <i>l</i>	CGCCI	AT CI	racgi rgato	CCTG	AT:	rcaa <i>i</i>	AGTC	ATTO	CCTC	rct (GCT	ACTTCA	1557
169 171 173 175 177	CTAA CTGC CTCT	AGCT! GTTT(IGCA(TAG A	395 AGGCO GAGAA GAGAO	CGCC# NACC# GATG(AT CI AT CI CT CI	TACGT TGAT(AGACT	CCTG(FGAT(C AT	rcaa <i>i</i>	AGTC	ATTO	CCTC	rct (GCT	ACTTCA	1557 1617
169 171 173 175 177	CTAA CTGC CTCT	AGCT! GTTT(IGCA(INF(TAG A	395 AGGCC GAGAA GAGAC FION	CGCCA AACCA GATGO FOR	AT CT AT CT CT CA SEQ	PACGI GATO AGACI ID I	CCTGC FGATC	C ATS	rcaa <i>i</i>	AGTC	ATTO	CCTC	rct (GCT	ACTTCA	1557 1617
169 171 173 175 177 180	CTAACTCTAA(2)	AGCT! GTTT(IGCA(INF(PAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCC GAGAA GAGAC FION	CGCCA AACCA GATGO FOR CE CI	AT CT AT CT CT CA SEQ HARAC	PACGI PGATO AGACI ID 1 CTERI	CCTG(FGAT(NO: 2	C ATT C AAC 2: CS:	rcaa <i>i</i> gacc <i>i</i>	AGTC	ATTO	CCTC	rct (GCT	ACTTCA	1557 1617
169 171 173 175 177 180 182	CTAA CTGC CTCT A (2)	AGCT! GTTT(IGCA(INF(TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCO GAGAO GAGAO GAGAO GUENO	CGCCA AACCA GATGO FOR CE CH	AT CT AT CT CT CA SEQ HARACH: 35	FACGT FGAT(AGACT ID 1 CTERI 98 an	CCTGC TGATC NO: 2 ISTIC	C ATT C AAC 2: CS:	rcaa <i>i</i> gacc <i>i</i>	AGTC	ATTO	CCTC	rct (GCT	ACTTCA	1557 1617
169 171 173 175 177 180 182 183	CTAA CTGG CTCT A (2)	AGCT! GTTT(IGCA(INF(TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCO GAGAA GAGAO PION QUENO A) LI	EGCCA AACCA FOR FOR EE CH ENGTH	AT CT AT CT CT CA SEQ HARAC H: 39	FACGT FGATO AGACT ID 1 CTERI 98 an	CCTGC TGATC NO: 2 ISTIC mino cid	C ATT C AAC 2: CS:	rcaa <i>i</i> gacc <i>i</i>	AGTC	ATTO	CCTC	rct (GCT	ACTTCA	1557 1617
169 171 173 175 177 180 182 183 184 185	CTAL CTGC CTCT A (2)	AGCTT GTTTC FGCAC INFC (ii	TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCC GAGAC FION QUENC A) LH B) TS C) TC LECUI	CGCCAACCAACCAACCAACCAACCAACCAACCAACCAAC	AT CT AT CT SEQ HARACH: 39 amin OGY:	TACGT TGATO AGACT ID 1 TCTERI 98 and according according to the control of the co	CCTGC FGATC NO: 2 ISTIC nino cid ear cein	C ATT C AAC CS: acid	rcaa <i>l</i> Gacc <i>l</i> ds	AGTC AGAA	ATTO GAA	CCTC	rct (GCT	ACTTCA	1557 1617
169 171 173 175 177 180 182 183 184 185 187	CTAA CTGC CTCT A (2)	AGCTTGGCAG	TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCC GAGAC FION QUENC A) LH B) TO CLECUI	CGCCAACCAACCAFOR FOR CE CHENGTH (PE: CPOLCACCACCACCACCACCACCACCACCACCACCACCACCAC	AT CT AT CT SEQ HARACH: 39 amin DGY:	TACGT TGATCAGACT ID 1 TTERI 108 and accade line protesting	CCTGC TGATC NO: 2 ISTIC nino cid ear tein ON: 5	C ATT	rcaa gacca ds	AGTC AGAA	ATTO GAAA	CCTC!	PCT (GGCTA	ACTTCA CCGGAC	1557 1617
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169 171 173 175 177 180 182 183 184 185 187 189 191	CTAACTCTCTA (2)	AGCTT GTTTC INFO (i) (ii) (ii)	TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCC GAGAN GAGAC FION QUENC A) LH B) TO D) TC LECUI QUENC Ser	FOR CE CHENGTH OPPOLICE TO Thr	SEQ HARACH: 39 amin OGY: VPE: Gly	IACGT IGATO AGACT ID 1 CTERI 98 an no ac line prot	CCTGC FGATC NO: 2 ISTIC nino cid ear cein ON: 9 Gly	C ATT	TCAAA GACCA ds ID NO Thr 10	AGTC AGAA D: 2: Ser	ATTO GAAA :	Cys	PCT (GAG /	ASP	ACTTCA CCGGAC	1557 1617
169 171 173 175 177 180 182 183 184 185 187 189 191 192	CTAACTCTCTA (2)	AGCTT GTTTC INFO (i) (ii) (ii)	TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCC GAGAN GAGAC FION QUENC A) LH B) TY C) TC LECUI QUENC Ser Ala	FOR CE CHENGTH OPPOLICE TO Thr	SEQ HARACH: 39 amin OGY: VPE: Gly	IACGT IGATO AGACT ID 1 CTERI 98 an no ac line prot	CCTGC FGATC NO: 2 ISTIC nino cid ear cein ON: 9 Gly	C ATT C AAC 2: CS: acic SEQ T Asn	TCAAA GACCA ds ID NO Thr 10	AGTC AGAA D: 2: Ser	ATTO GAAA	Cys	SAG A	ASP	ACTTCA CCGGAC	1557 1617
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169 171 173 175 177 180 182 183 184 185 187 199 191 192 194 195 197	CTAACTCTCTAA (2) Met 1 Leu Ser	AGCTTGCAG INFO (ii (xi Asp Ala	TAG A CCT (CAT (395 AGGCO GAGAN GION QUENC A) LH B) TO CUENC Ser Ala 20 Asp	FOR CE CHENGTH OPOLICE TYPE: Thr Ser Gly	SEQ HARACH: 39 amin OGY: (PE: ESCR: Gly Cys	IACGT IGATO AGACT ID I CTERI 88 an 10 ac 1ine prot IPTIC Pro Ser Gln	CCTGC CGATC NO: 2 ISTIC nino cid ear cein DN: 9 Gly Pro Ser 40	C ATT C AAC 2: CS: acid SEQ T Asn Ala 25 Asp	ID NO Thr 10 Pro	AGTC AGAA Ser Gly Cys	ATTO GAAA : Asp Ser Gly	Cys Trp Leu 45	Ser Leu 30 Asn	Asp 15 Asn Arg	ACTTCA CCGGAC Pro Leu Thr	1557 1617
169 171 173 175 177 180 182 183 184 185 187 199 191 192 194 195 197 198 200	CTAACTCTCTAA (2) Met 1 Leu Ser	AGCTTGCAG INFG (ii (xi Asp Ala His	TAG A CCT (CAT (395 AGGCO GAGAN GION QUENC A) LH B) TO CUENC Ser Ala 20 Asp	FOR CE CHENGTH OPOLICE TYPE: Thr Ser Gly	SEQ HARACH: 39 amin OGY: (PE: ESCR: Gly Cys	IACGT IGATO AGACT ID I OTER: 88 an 10 ac 1ine prot Pro Ser Gln Ser	CCTGC CGATC NO: 2 ISTIC nino cid ear cein DN: 9 Gly Pro Ser 40	C ATT C AAC 2: CS: acid SEQ T Asn Ala 25 Asp	ID NO Thr 10 Pro	AGTC AGAA Ser Gly Cys	ATTO GAAA Asp Ser Gly Thr	Cys Trp Leu 45	Ser Leu 30 Asn	Asp 15 Asn Arg	ACTTCA CCGGAC Pro Leu Thr	1557 1617
169 171 173 175 177 180 182 183 184 185 187 199 191 192 194 195 197 198 200 201	CTAM CTGC CTCTA (2)	AGCTTGCAG INFG (ii (xi Asp Ala His Leu 50	TAG A CCT (CAT (395 AGGCO GAGAO FION QUENCA) LI B) TO LECUI QUENC Ser Ala 20 Asp	FOR CE CHENGTH (PE: DPOLCE TY SET Gly Asn	SEQ HARACHERS GLY CYS Asn Asp	IACGT IGATO AGACT ID 1 OTER: 98 an 10 ac 1ine prot Pro Ser Gln Ser 55	CCTGC CGATC NO: 2 ISTIC nino cid ear cein ON: 5 Gly Pro Ser 40 Leu	C ATT C AAC 2: CS: acid Asn Ala 25 Asp Cys	TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGTC AGAA O: 2 Ser Gly Cys Gln	ATTO GAAA	Cys Trp Leu 45	Ser Leu 30 Asn Ser	Asp 15 Asn Arg	Pro Leu Thr	1557 1617
169 171 173 175 177 180 182 183 184 185 187 199 191 192 194 195 197 198 200 201 203	CTAACTOCAA (2) Met 1 Leu Ser Gly Met	AGCTTGCAG INFG (ii (xi Asp Ala His Leu 50	TAG A CCT (CAT (395 AGGCO GAGAO FION QUENCA) LI B) TO LECUI QUENC Ser Ala 20 Asp	FOR CE CHENGTH (PE: DPOLCE TY SET Gly Asn	SEQ HARACH: 39 amin OGY: VPE: ESCRI Gly Cys Asn Asp	IACGT IGATO AGACT ID 1 OTER: 98 an 10 ac 1ine prot Pro Ser Gln Ser 55	CCTGC CGATC NO: 2 ISTIC nino cid ear cein ON: 5 Gly Pro Ser 40 Leu	C ATT C AAC 2: CS: acid Asn Ala 25 Asp Cys	TCAAA GACCA ds ID NO Thr 10 Pro Pro	AGTC AGAA O: 2 Ser Gly Cys Gln Tyr	ATTO GAAA Asp Ser Gly Thr	Cys Trp Leu 45	Ser Leu 30 Asn Ser	Asp 15 Asn Arg	Pro Leu Thr Ser	1557 1617
169 171 173 175 177 180 182 183 184 185 187 191 192 194 195 197 198 200 201 203 204	CTAACTOCAA (2) Met 1 Leu Ser Gly Met 65	AGCTTGCAG INFO (ii (xi Asp Ala His Leu 50 Val	TAG ACCT (CAT (CAT (CAT (CAT (CAT (CAT (CAT	395 AGGCC GAGAM GAGAC FION QUENC B) TO LECUI QUENC Ser Ala 20 Asp Gly Ala	FOR CE CHENGTH OPOLO Thr 5 Ser Gly Asn	SEQ HARACH: 39 amin OGY: VPE: ESCR: Gly Cys Asn Asp	IACGT GATO AGACT ID 1 CTERI 98 and acc line prot Pro Ser Gln Ser 55 Ile	CCTGC CGATC NO: 2 ISTIC nino cid ear cein ON: 3 Gly Pro Ser 40 Leu Met	C ATT C AAC 2: CS: acic Asn Ala 25 Asp Cys	ID NO Thr 10 Pro Pro Leu	Cys Gln Tyr 75	ATTO GAAA	Cys Trp Leu 45 Gly	Ser Leu 30 Asn Ser Val	Asp 15 Asn Arg Pro	Pro Leu Thr Ser Val 80	1557 1617

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218 Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
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230 Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
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233 Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
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236 Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
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239 Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
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242 Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
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245 Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
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248 Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
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249 305
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251 Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
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264 385
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267 (2) INFORMATION FOR SEQ ID NO: 3:
         (i) SEQUENCE CHARACTERISTICS:
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              (A) LENGTH: 1618 base pairs
271
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
272
              (D) TOPOLOGY: linear
273
276
        (ix) FEATURE:
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              (A) NAME/KEY: CDS
278
              (B) LOCATION: 339..1232
281
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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287	GCT	TGAC	GAG (GAAG	AGGC:	rg go	GCG	CGTGC	AAC	CCCG	AAA	GTC	rgag1	rgc :	rctc.	AGTTAC	180
289	AGC	CTAC	CTA (GTCC	GCAG	CA GO	CCT	CAGO	ACC	CATG	BACA	GCAG	CAC	CGG (CCCA	GGAAC	240
291	ACC	AGCGZ	ACT	GCTC	AGAC	CC CI	TAGO	CTCAC	GC	AAGT:	rgct	ccc	CAGC	ACC !	rggc:	rcctgg	300
				CCCA													353
294													rg Se	_	_		
295												1	- 5 - 1			5	
	CAC	ccc	CCT	TGG	ccc	CDD	CCA	CAG	ССТ	стс	CCC	_	GAC	ccc	CAG		401
				Trp													101
299	1113	пта	лта	ттр	10	Giu	пту	GIII	110	15	110	DCI	пор	111 9	20	110	
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				CCT													497
	Cys	ser		Pro	ьeu	Arg	гла		Pro	GTA	HIS	vaı		Asp	Cys	гĀг	
307			40					45					50				
				AAT													545
310	Ile	His	Gln	Asn	Glu	Asp		His	Gln	His	Leu		Phe	Gln	Pro	Cys	
311		55					60					65					
				CGC													593
314	Ser	Gly	Arg	Arg	Leu	Ser	Asp	Gln	Tyr	Thr	Ala	Leu	Ser	Glu	Cys	Gln	
315	70					75					80					85	
317	CTA	CCT	GAT	GGG	AAC	ATG	GCC	CTT	CGG	AAC	CAT	CCT	CTG	CAA	GAT	CGT	641
318	Leu	Pro	Asp	Gly	Asn	Met	Ala	Leu	Arg	Asn	His	Pro	Leu	Gln	Asp	Arg	
319			_	_	90				•	95					100		
321	GAT	CTC	AAT	AGA	TTA	CTA	CAA	CAT	GTT	CAC	CAG	CAT	ATT	CAC	CCT	CTG	689
				Arg													
323	•			105					110					115			
	CAC	САТ	GAG	CGT	GGA	ĊCG	СТА	CAT		TGT	CTG	CCA	CCC	AGT	CAA	AGC	737
				Arg													
327			120	5	1			125	-1-	-1-			130				
	ССТ	GGA		CCG	TAC	CCC	CCG		TGC	CAA	аат	CGT		CGT	CTG	CAA	785
				Pro													
331	110	135	1110	110	-1-	110	140	2,5	0,0	01	11011	145	01	*** 9	Lou	01	
	CTG		ССТ	CTC	ጥጥረ	ጥርር		ccc	тСт	GCC	ጥርጥ		СТТ	СΣΨ	GGC	AAC	833
				Leu													033
	150	ASP	PIO	ьец	FILE	155	nis	AIG	261	Ата	160	ASII	vai	1112	Gry	165	
		222	3 (1) 3	CA C	CON		CMC	C 3 III	202	mmc		CCIII	C3 C	cmm	CMC.		881
				CAG													001
	HIS	гаг	TTE	Gln		GTĀ	val	HIS	Arg			Pro	HIS	vaı		PIO	
339			ama		170			aam	a a m	175		ama	mam	~mm	180	amm	020
				GTA													929
	Pro	Asn	Leu	Val	ьęи	GLY	GLu	Pro		GIn	Asn	Leu	Cys		тyr	ьeu	
343				185					190					195			
				CAT													977
	Arg	Phe		His	Ala	Asp	Pro		His	His	Cys	Val		Arg	Pro	Asp	
347			200					205					210				
				ACT													1025
350	Asp	Leu	Thr	Thr	Gln	Glu	Arg	Ser	His	Ala	Ile	Gly	Leu	Gln	Arg	Lys	

VERIFICATION SUMMARY

DATE: 12/05/2001

PATENT APPLICATION: US/09/841,720A

TIME: 15:07:26

Input Set : N:\Crf3\RULE60\09841720A.RAW
Output Set: N:\CRF3\12052001\1841720A.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]